IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:	)	Examiner: Angell, Jon E.
Avi J. ASHKENAZI, et al..	)	Art Unit: 1635
Application Serial No. 09/978,564	)	Confirmation No. 5282
Filed: October 16, 2001	)	Attorney's Docket No. 39780-2630 P1C25
For: **SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME**	)	**Customer No. 35489**

DECLARATION OF DR. LUC DESNOYERS, DR. AUDREY GODDARD, DR. PAUL J. GODOWSKI, DR. AUSTIN GURNEY and DR. WILLIAM I. WOOD, UNDER 37 C.F.R. §1.131

MAIL STOP AMENDMENT
Commissioner for Patents
P.O. Box 1450
Alexandria, Virginia 22313-1450

Dear Sir:

We, Luc Desnoyers, Ph.D., Audrey Goddard, Ph.D., Paul J. Godowski, Ph.D., Austin Gurney, Ph.D. and William I. Wood, Ph.D. declare and say as follows:

1. We are the inventors of the above-identified application. We have read and understood the claims pending in this application, and are aware that the claims stand rejected as allegedly being unpatentable over Holtzman *et al.*, U.S. 2002/0055139, published May 9, 2002 with priority to May 14, 1999. Holtzman *et al.* teach a polypeptide (human A236 protein) that is 100% identical to SEQ ID NO:59.

2. The polypeptide designated as PRO363 (SEQ ID NO:59), antibodies to which are claimed in the above-identified application, was sequenced, cloned and identified as having homology to the cell surface protein HCAR in the United States prior to May 14,1999.

3. U.S. Provisional Application No. 60/078,910, filed on March 20, 1998, discloses sequences designated as SEQ ID NO:1 and SEQ ID NO:3. The native sequence polypeptide of SEQ ID NO:3 is identical to SEQ ID NO:59 of the above-identified application, while SEQ ID

NO:1 is identical to SEQ ID NO:58 of the above-identified application. A copy of U.S. Provisional Application No. 60/078,910 is enclosed as **Exhibit A**.

4. U.S. Provisional Application No. 60/078,910, filed on March 20, 1998 further discloses that SEQ ID NO:3, corresponding to SEQ ID NO:59 of the above-identified application, has homology to the cell surface protein HCAR.

5. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

Luc Desnoyers, Ph.D.	Date
Audrey Goddard, Ph.D.	Date
Paul J. Godowski, Ph.D.	Date
Austin Gurney, Ph.D.	Date
William I. Wood, Ph.D.	Date

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NOVEL POLYPEPTIDES HAVING HOMOLOGY TO THE CELL SURFACE PROTEIN HCAR AND NUCLEIC ACIDS ENCODING THE SAME

FIELD OF THE INVENTION

The present invention relates generally to the identification and isolation of novel DNA and to the recombinant production of novel polypeptides having homology to the cell surface protein HCAR, designated herein as "PRO363" polypeptides.

BACKGROUND OF THE INVENTION

Membrane-bound proteins and receptors can play an important role in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. Such membrane-bound proteins and cell receptors include, but are not limited to, cytokine receptors, receptor kinases, receptor phosphatases, receptors involved in cell-cell interactions, and cellular adhesin molecules like selectins and integrins. For instance, transduction of signals that regulate cell growth and differentiation is regulated in part by phosphorylation of various cellular proteins. Protein tyrosine kinases, enzymes that catalyze that process, can also act as growth factor receptors. Examples include fibroblast growth factor receptor and nerve growth factor receptor.

Membrane-bound proteins and receptor molecules have various industrial applications, including as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be employed as therapeutic agents to block receptor-ligand interaction. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

The cell surface protein HCAR is a membrane-bound protein that acts as a receptor for subgroup C of the adenoviruses and subgroup B of the coxsackieviruses. Thus, HCAR may

provide a means for mediating viral infection of cells in that the presence of the HCAR receptor on the cellular surface provides a binding site for viral particles, thereby facilitating viral infection.

In light of the physiological importance of membrane-bound proteins and spcficially those which serve a cell surface receptor for viruses, efforts are currently being undertaken by both industry and academia to identify new, native membrane-bound reeptor proteins. Many of these efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor proteins. We herein describe a novel membrane-bound polypeptide having homology to the cell surface protein HCAR and to various tumor antigens including A33 and carcinoembryonic antigen, wherein this polypeptide may be a novel cell surface virus receptor or tumor antigen.

SUMMARY OF THE INVENTION

Applicants have identified a cDNA clone that encodes a novel polypeptide having homology to the cell surface receptor protein HCAR, wherein the polypeptide is designated in the present application as "PRO363".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO363 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO363 polypeptide having amino acid residues 1 to 373 of Figure 2 (SEQ ID NO:3), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. In another aspect, the isolated nucleic acid comprises DNA encoding a PRO363 extracellular domain polypeptide having amino acid residues 1 to X of Figure 2 (SEQ ID NO:3) where X is any amino acid from amino acid 216 to amino acid 225, or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. The isolated nucleic acid sequence may comprise the cDNA insert of the DNA45419-1252 vector deposited on February 5, 1998 as ATCC ____________ which includes the nucleotide sequence encoding PRO363.

In another embodiment, the invention provides a vector comprising DNA encoding a PRO363 polypeptide. A host cell comprising such a vector is also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing PRO363 polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of PRO363 and recovering PRO363 from the cell culture.

In another embodiment, the invention provides isolated PRO363 polypeptide. In particular, the invention provides isolated native sequence PRO363 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 373 of Figure 2 (SEQ ID NO:3). An additional embodiment of the present invention is directed to an isolated extracellular domain of a PRO363 polypeptide, wherein that extracellular domain may comprise amino acids 1 to X of the sequence shown in Figure 2 (SEQ ID NO:3), where X is any amino acid from amino acid 216 to 225. Optionally, the PRO363 polypeptide is obtained or is obtainable by expressing the polypeptide encoded by the cDNA insert of the DNA45419-1252 vector deposited on February 5, 1998 as ATCC ___________________.

In another embodiment, the invention provides chimeric molecules comprising a PRO363 polypeptide or extracellular domain thereof fused to a heterologous polypeptide or amino acid sequence. An example of such a chimeric molecule comprises a PRO363 polypeptide fused to an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which specifically binds to a PRO363 polypeptide or extracellular domain thereof. Optionally, the antibody is a monoclonal antibody.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A-C show a nucleotide sequence (SEQ ID NO:1) containing the nucleotide sequence (SEQ ID NO:2) of a native sequence PRO363 cDNA (nucleotides), wherein the nucleotide sequence (SEQ ID NO:1) is a clone designated herein as "UNQ318" and/or "DNA45419-1252". Also presented is the position of the initiator methionine residue. The deduced amino acid sequence of the encoded PRO363 polypeptide is shown below the nucleotide sequence.

Figure 2 shows the amino acid sequence (SEQ ID NO:3) derived from nucleotides 190-1308 of the nucleotide sequence shown in Figure 1. Also shown in Figure 2 as underlined is the location of the transmembrane domain for the full-length PRO363 polypeptide.

Figures 3A-B show an alignment of nucleotide sequences from a variety of expressed sequence tags as well as a consensus nucleotide sequence derived therefrom designated "<consen01>". The <consen01> consensus nucleotide sequence is also herein designated as DNA42828.

Figure 4 shows a double-stranded representation of the DNA42828 sequence shown in Figures 3A-B. Also shown in Figure 4 as underlined are the locations of three oligonucleotide

primers based upon the DNA42828 sequence designated "42828.f1", "42828.r1" and "42828.p1".

Figure 5 shows homology between the amino acid sequences designated MYP0_BOVIN and MYP0_HUMAN and the amino acid sequence encoded by DNA45419-1252 evidencing that the polypeptide encoded by DNA45419-1252 possesses myelin P0 protein domains.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

The terms "PRO363 polypeptide" and "PRO363" when used herein encompass native sequence PRO363 and PRO363 polypeptide variants (which are further defined herein). The PRO363 polypeptides may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods.

A "native sequence PRO363 polypeptide" comprises a polypeptide having the same amino acid sequence as a PRO363 polypeptide derived from nature. Such native sequence PRO363 polypeptide can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO363 polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of a PRO363 polypeptide (*e.g.*, soluble forms containing for instance, an extracellular domain sequence), naturally-occurring variant forms (*e.g.*, alternatively spliced forms) and naturally-occurring allelic variants of a PRO363 polypeptide. In one embodiment of the invention, the native sequence PRO363 polypeptide is a mature or full-length native sequence PRO363 polypeptide comprising amino acids 1 to 373 of Figure 2 (SEQ ID NO:3). In another embodiment of the invention, the native sequence PRO363 polypeptide is an extracellular domain of the full-length PRO363 protein that comprises amino acids 1 to X of the amino acid sequence shown in Figure 2 (SEQ ID NO:3), wherein X is any amino acid from amino acid 216 to 225. Optionally, the PRO363 polypeptide is obtained or obtainable by expressing the polypeptide encoded by the cDNA insert of the vector DNA45419-1252 deposited on February 5, 1998 as ATCC ____________________.

The "PRO363 extracellular domain" or "PRO363 ECD" refers to a form of the PRO363 polypeptide which is essentially free of the transmembrane and cytoplasmic domains of the PRO363 polypeptide. Ordinarily, PRO363 ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. Optionally, PRO363 polypeptide ECD will comprise amino acid residues 1 to X of Figure 2 (SEQ ID NO:3). It will be understood that any transmembrane domain identified for

the PRO363 polypeptide of the present invention is identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified. Accordingly, the PRO363 polypeptide ECD may optionally comprise amino acids 1 to X of Figure 2 (SEQ ID NO:3), wherein X is any one of amino acid residues 216 to 225 of Figure 2 (SEQ ID NO:3).

"PRO363 variant" means an active PRO363 polypeptide as defined below having at least about 80% amino acid sequence identity with the PRO363 polypeptide having the deduced amino acid sequence shown in Figure 2 (SEQ ID NO:3) for a full-length native sequence PRO363 polypeptide. Such PRO363 polypeptide variants include, for instance, PRO363 polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the sequence of Figure 2 (SEQ ID NO:3). Ordinarily, a PRO363 polypeptide variant will have at least about 80% amino acid sequence identity, preferably at least about 85% amino acid sequence identity, more preferably at least about 90% amino acid sequence identity and even more preferably at least about 95% amino acid sequence identity with the amino acid sequence of Figure 2 (SEQ ID NO:3).

"Percent (%) amino acid sequence identity" with respect to the PRO363 amino acid sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in a PRO363 polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

"Percent (%) nucleic acid sequence identity" with respect to the PRO363 sequence identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO363 sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as ALIGN or Megalign (DNASTAR) software. Those skilled in the art can

determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

The term "epitope tagged" where used herein refers to a chimeric polypeptide comprising a PRO363 polypeptide, or domain sequence thereof, fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody may be made, or which can be identified by some other agent, yet is short enough such that it does not interfere with the activity of the PRO363 polypeptide. The tag polypeptide preferably is also fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 to about 50 amino acid residues (preferably, between about 10 to about 20 residues).

"Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the PRO363 polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" PRO363 polypeptide-encoding nucleic acid molecule is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the PRO363 polypeptide-encoding nucleic acid. An isolated PRO363 polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated PRO363 polypeptide-encoding nucleic acid molecules therefore are distinguished from the PRO363 polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated PRO363 polypeptide-encoding nucleic acid molecule includes PRO363 polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express PRO363 polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The term "antibody" is used in the broadest sense and specifically covers single anti-PRO363 polypeptide monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies) and anti-PRO363 antibody compositions with polyepitopic specificity. The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

"Active" or "activity" for the purposes herein refers to form(s) of PRO363 which retain the biologic and/or immunologic activities of native or naturally-occurring PRO363 polypeptide.

The terms “treating”, “treatment” and “therapy” as used herein refer to curative therapy, prophylactic therapy, and preventative therapy.

The term “mammal” as used herein refers to any mammal classified as a mammal, including humans, cows, horses, dogs and cats. In a preferred embodiment of the invention, the mammal is a human.

II. Compositions and Methods of the Invention

A. Full-length PRO363 Polypeptide

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO363. In particular, Applicants have identified and isolated cDNA encoding a PRO363 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO363 polypeptide has significant similarity to the cell surface protein HCAR. Accordingly, it is presently believed that PRO363 polypeptide disclosed in the present application is a newly HCAR homolog.

B. PRO363 Variants

In addition to the full-length native sequence PRO363 polypeptide described herein, it is contemplated that PRO363 variants can be prepared. PRO363 variants can be prepared by introducing appropriate nucleotide changes into the PRO363-encoding DNA, or by synthesis of the desired PRO363 polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO363 polypeptide, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

Variations in the native full-length sequence PRO363 or in various domains of the PRO363 polypeptide described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO363 polypeptide that results in a change in the amino acid sequence of the PRO363 polypeptide as compared with the native sequence PRO363. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO363 polypeptide. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the PRO363 polypeptide with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of

amino acids in the sequence and testing the resulting variants for activity in any of the *in vitro* assays described in the Examples below.

The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al., Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO363-encoding variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

C. Modifications of PRO363

Covalent modifications of PRO363 polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO363 polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of a PRO363 polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO363 to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO363 antibodies, and vice-versa. Commonly used crosslinking agents include, *e.g.*, 1,1-bis(diazo-acetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the

α-amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the PRO363 polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO363 polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence PRO363 polypeptide.

Addition of glycosylation sites to PRO363 polypeptides may be accomplished by altering the amino acid sequence thereof. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO363 polypeptide (for O-linked glycosylation sites). The PRO363 amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the PRO363 polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO363 polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the PRO363 polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of PRO363 comprises linking the PRO363 polypeptide to one of a variety of nonproteinaceous polymers, *e.g.*, polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

PRO363 polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a PRO363 polypeptide fused to another, heterologous

polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a PRO363 polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the PRO363 polypeptide. The presence of such epitope-tagged forms of a PRO363 polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO363 polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a PRO363 polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an α-tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

The PRO363 polypeptide of the present invention may also be modified in a way to form a chimeric molecule comprising a PRO363 polypeptide fused to a leucine zipper. Various leucine zipper polypeptides have been described in the art. See, e.g., Landschulz et al., Science 240:1759 (1988); WO 94/10308; Hoppe et al., FEBS Letters 344:1991 (1994); Maniatis et al., Nature 341:24 (1989). It is believed that use of a leucine zipper fused to a PRO363 polypeptide may be desirable to assist in dimerizing or trimerizing soluble PRO363 polypeptide in solution. Those skilled in the art will appreciate that the leucine zipper may be fused at either the N- or C-terminal end of the PRO363 molecule.

D. Preparation of PRO363

The description below relates primarily to production of PRO363 by culturing cells transformed or transfected with a vector containing PRO363 polypeptide encoding nucleic

acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO363 polypeptides. For instance, the PRO363 sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of PRO363 polypeptides may be chemically synthesized separately and combined using chemical or enzymatic methods to produce a full-length PRO363 polypeptide.

1. Isolation of DNA Encoding PRO363

DNA encoding a PRO363 polypeptide may be obtained from a cDNA library prepared from tissue believed to possess the PRO363 mRNA and to express it at a detectable level. Accordingly, human PRO363-encoding DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO363-encoding gene may also be obtained from a genomic library or by oligonucleotide synthesis.

Libraries can be screened with probes (such as antibodies to a PRO363 polypeptide or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO363 is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer:A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ^{32}P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other

private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined through sequence alignment using computer software programs such as ALIGN, DNAstar, and INHERIT which employ various algorithms to measure homology.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for PRO363 polypeptide production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of transfection are known to the ordinarily skilled artisan, for example, $CaPO_4$ and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes or other cells that contain substantial cell-wall barriers. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transformations have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, *e.g.*, polybrene, polyornithine, may also be used. For various techniques for transforming

mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635).

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO363-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism.

Suitable host cells for the expression of glycosylated PRO363 are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as Drosophila S2 and Spodoptera Sf9, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol., 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

3. Selection and Use of a Replicable Vector

The nucleic acid (*e.g.*, cDNA or genomic DNA) encoding the desired PRO363 polypeptide may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more

of these components employs standard ligation techniques which are known to the skilled artisan.

The desired PRO363 polypeptide may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO363-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, *e.g.*, the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α-factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, *e.g.*, ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, *e.g.*, the gene encoding D-alanine racemase for *Bacilli*.

An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO363-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp*1 gene present in the yeast plasmid YRp7 [Stinchcomb et al., Nature, 282:39 (1979); Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)]. The *trp*1 gene

provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, Genetics, 85:12 (1977)].

Expression and cloning vectors usually contain a promoter operably linked to the PRO363-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β-lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (trp) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid promoters such as the tac promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding the PRO363 polypeptide.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., J. Biol. Chem., 255:2073 (1980)] or other glycolytic enzymes [Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

PRO363 transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, *e.g.*, the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding a PRO363 polypeptide by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription.

Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α-fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO363 coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO363.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO363 polypeptides in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.

4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO363 polypeptide or against a synthetic peptide based

on the DNA sequences provided herein or against exogenous sequence fused to PRO363-encoding DNA and encoding a specific antibody epitope.

5. Purification of Polypeptide

Forms of PRO363 may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (*e.g.* Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO363 polypeptides can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify PRO363 from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO363 polypeptide. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification:Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO363 polypeptide produced.

E. Uses for PRO363

Nucleotide sequences (or their complement) encoding PRO363 polypeptides have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO363-encoding nucleic acid will also be useful for the preparation of PRO363 polypeptides by the recombinant techniques described herein.

The full-length DNA45419-1252 nucleotide sequence (SEQ ID NO:1) or the full-length native sequence PRO363 (SEQ ID NO:2) nucleotide sequence, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length PRO363 gene or to isolate still other genes (for instance, those encoding naturally-occurring variants of PRO363 or PRO363 from other species) which have a desired sequence identity to the PRO363 nucleotide sequence disclosed in Figure 1 (SEQ ID NO:1). Optionally, the length of the

probes will be about 20 to about 50 bases. The hybridization probes may be derived from the UNQ318 (DNA45419-1252) nucleotide sequence of SEQ ID NO:1 as shown in Figure 1 or from genomic sequences including promoters, enhancer elements and introns of native sequence PRO363-encoding DNA. By way of example, a screening method will comprise isolating the coding region of the PRO363 gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, including radionucleotides such as ^{32}P or ^{35}S, or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the PRO363 gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO363 sequences.

Nucleotide sequences encoding a PRO363 polypeptide can also be used to construct hybridization probes for mapping the gene which encodes that PRO363 polypeptide and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

When the coding sequences for PRO363 encode a protein which binds to another protein (example, where the PRO363 polypeptide functions as a receptor), the PRO363 polypeptide can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor PRO363 polypeptide can be used to isolate correlative ligand(s). Screening assays can be designed to find lead compounds that mimic the biological activity of a native PRO363 or a receptor for PRO363. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

Nucleic acids which encode PRO363 polypeptide or any of its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding PRO363 polypeptide can be used to clone genomic DNA encoding PRO363 in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding PRO363. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for PRO363 transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding PRO363 introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding PRO363. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of PRO363 can be used to construct a PRO363 "knock out" animal which has a defective or altered gene encoding PRO363 as a result of homologous recombination between the endogenous gene encoding PRO363 and altered genomic DNA encoding PRO363 introduced into an embryonic cell of the animal. For example, cDNA encoding PRO363 can be used to clone genomic DNA encoding PRO363 in accordance with established techniques. A portion of the genomic DNA encoding PRO363 can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, Cell, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., Cell, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in

Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the PRO363 polypeptide.

PRO363 polypeptides of the present invention which possess biological activity related to that of the cell surface HCAR protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO363 polypeptides of the present invention for such purposes. Specifically, extracellular domains derived from the PRO363 polypeptides may be employed therapeutically *in vivo* for lessening the effects of viral infection.

F. Anti-PRO363 Antibodies

The present invention further provides anti-PRO363 polypeptide antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

The anti-PRO363 antibodies of the present invention may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO363 polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

2. Monoclonal Antibodies

The anti-PRO363 antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the PRO363 polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Rockville, Maryland. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against a PRO363 polypeptide. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or

enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, supra]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., supra] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

3. Humanized Antibodies

The anti-PRO363 antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human

species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et al., J. Immunol., 147(1):86-95 (1991)].

4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for a PRO363 polypeptide, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, Nature, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., EMBO J., 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

5. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

G. Uses for anti-PRO363 Antibodies

The anti-PRO363 antibodies of the present invention have various utilities. For example, anti-PRO363 antibodies may be used in diagnostic assays for PRO363 polypeptides, *e.g.*, detecting expression in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, Monoclonal Antibodies: A Manual of Techniques, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as ^{3}H, ^{14}C, ^{32}P, ^{35}S, or ^{125}I, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Anti-PRO363 antibodies also are useful for the affinity purification of PRO363 polypeptides from recombinant cell culture or natural sources. In this process, the antibodies against a PRO363 polypeptide are immobilized on a suitable support, such a Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the PRO363 polypeptide to be purified, and thereafter the

support is washed with a suitable solvent that will remove substantially all the material in the sample except the PRO363 polypeptide, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the PRO363 polypeptide from the antibody.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Rockville, Maryland.

EXAMPLE 1: Isolation of cDNA Clones Encoding Human PRO363

The extracellular domain (ECD) sequences (including the secretion signal, if any) of from about 950 known secreted proteins from the Swiss-Prot public protein database were used to search expressed sequence tag (EST) databases. The EST databases included public EST databases (e.g., GenBank) and a proprietary EST DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequence. Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Washington; http://bozeman.mbt.washington.edu/phrap.docs/phrap.html).

A consensus DNA sequence was assembled relative to other EST sequences using phrap. This consensus sequence is herein designated DNA42828 (see Figures 3A-B and 4). Based on the DNA42828 consensus sequence shown in Figures 3A-B and 4, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO363. Forward and reverse PCR primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe

sequences are typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel et al., Current Protocols in Molecular Biology, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer (42828.f1) 5'-CCAGTGCACAGCAGGCAACGAAGC-3' (SEQ ID NO:4)

reverse PCR primer (42828.r1) 5'-ACTAGGCTGTATGCCTGGGTGGGC-3' (SEQ ID NO:5)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA42828 sequence which had the following nucleotide sequence

hybridization probe (42828.p1)
5'-GTATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGC-3' (SEQ ID NO:6)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO363 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227). The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO363 [herein designated as UNQ318 (DNA45419-1252)] (SEQ ID NO:1) and the derived protein sequence for PRO363.

The entire nucleotide sequence of UNQ318 (DNA45419-1252) is shown in Figure 1 (SEQ ID NO:1). Clone UNQ318 (DNA45419-1252) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 190-192 [Kozak et al., supra] and ending at the stop codon at nucleotide positions 1309-1311 (Figure 1). The predicted polypeptide precursor is 373 amino acids long (Figure 2). The full-length PRO363 protein shown in Figure 2 has an estimated molecular weight of about 41,281 daltons and a pI of about 8.33. A transmembrane domain exists at amino acids 221 to 254 of the amino acid sequence shown in Figure 2 (SEQ ID NO:3). The PRO363 polypeptide possesses at least two myelin P0 protein domains as shown in Figure 5. Clone UNQ318 (DNA45419-1252) has been deposited with ATCC on February 5, 1998 and is assigned ATCC deposit no. ____________ ________.

Analysis of the amino acid sequence of the full-length PRO363 polypeptide suggests that it possesses significant sequence similarity to the cell surface protein HCAR, thereby indicating that PRO363 may be a novel HCAR homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO363 amino acid sequence and the following Dayhoff sequences, HS46KDA_1, HSU90716_1, MMCARH_1, MMCARHOM_1, MMU90715_1, A33_HUMAN, P_W14146, P_W14158, A42632 and B42632.

EXAMPLE 2: Use of PRO363-encoding DNA as a hybridization probe

The following method describes use of a nucleotide sequence encoding PRO363 as a hybridization probe.

DNA comprising the coding sequence of full-length PRO363 (as shown in Figure 1, SEQ ID NO:1) or a fragment thereof is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO363) in human tissue cDNA libraries or human tissue genomic libraries.

Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO363 polypeptide-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO363 polypeptide can then be identified using standard techniques known in the art.

EXAMPLE 3: Expression of PRO363 Polypeptides in *E. coli*

This example illustrates the preparation of unglycosylated forms of PRO363 polypeptides by recombinant expression in *E. coli*.

The DNA sequence encoding the full-length PRO363 polypeptide or a fragment or variant thereof is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO363 coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO363 polypeptide can then be purified using a metal chelating column under conditions that allow tight binding of the polypeptide.

EXAMPLE 4: Expression of PRO363 Polypeptides in Mammalian Cells

This example illustrates preparation of glycosylated forms of PRO363 polypeptides by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the PRO363-encoding DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO363-encoding DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-PRO363.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 μg pRK5-PRO363 DNA is mixed with about 1 μg DNA encoding the VA RNA gene [Thimmappaya et al., Cell, 31:543 (1982)] and dissolved in 500 μl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M $CaCl_2$. To this mixture is added, dropwise, 500 μl of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM $NaPO_4$, and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 μCi/ml ^{35}S-cysteine and 200 μCi/ml ^{35}S-methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO363 polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, PRO363-encoding DNA may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., Proc. Natl. Acad. Sci., 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μg pRK5-PRO363 DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 μg/ml bovine insulin and 0.1 μg/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO363 polypeptide can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, PRO363 polypeptide can be expressed in CHO cells. The pRK5-PRO363 vector can be transfected into CHO cells using known reagents such as $CaPO_4$ or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ^{35}S-methionine. After determining the presence of PRO363 polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO363 polypeptide can then be concentrated and purified by any selected method.

Epitope-tagged PRO363 polypeptide may also be expressed in host CHO cells. The PRO363-encoding DNA may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO363-encoding DNA insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO363 polypeptide can then be concentrated and purified by any selected method, such as by Ni^{2+}-chelate affinity chromatography.

EXAMPLE 5: Expression of a PRO363 Polypeptide in Yeast

The following method describes recombinant expression of PRO363 polypeptides in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO363 polypeptide from the ADH2/GAPDH promoter. DNA encoding the PRO363 polypeptide of interest, a selected signal peptide and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of the PRO363 polypeptide. For secretion, DNA encoding the PRO363 polypeptide can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, the yeast alpha-factor secretory signal/leader sequence, and linker sequences (if needed) for expression of the PRO363 polypeptide.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant PRO363 polypeptide can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing the PRO363 polypeptide may further be purified using selected column chromatography resins.

EXAMPLE 6: Expression of PRO363 Polypeptides in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO363 polypeptides in Baculovirus-infected insect cells.

The PRO363-encoding DNA is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the PRO363-encoding DNA or the desired portion of the PRO363-encoding DNA (such as the sequence encoding the extracellular domain of a transmembrane protein) is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 to 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression is performed as described by O'Reilley et al., Baculovirus expression vectors: A laboratory Manual, Oxford:Oxford University Press (1994).

Expressed poly-his tagged PRO363 polypeptide can then be purified, for example, by Ni^{2+}-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM $MgCl_2$; 0.1 mM EDTA; 10% Glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% Glycerol, pH 7.8) and filtered through a 0.45 μm filter. A Ni^{2+}-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A_{280} with loading buffer, at which point fraction

collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% Glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A_{280} baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or western blot with Ni^{2+}-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His_{10}-tagged PRO363 polypeptide are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO363 polypeptide can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

EXAMPLE 7: Preparation of Antibodies that Bind PRO363 Polypeptides

This example illustrates the preparation of monoclonal antibodies which can specifically bind to PRO363 polypeptides.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified PRO363 polypeptide, fusion proteins containing a PRO363 polypeptide, and cells expressing recombinant PRO363 polypeptide on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the PRO363 immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO363 polypeptide antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO363 polypeptide. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and

thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against PRO363 polypeptide. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against a PRO363 polypeptide is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO363 polypeptide monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

Deposit of Material

The following materials have been deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD, USA (ATCC):

Material	ATCC Dep. No.	Deposit Date
DNA45419-1252		February 5, 1998

This deposit was made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposit will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC §122 and the Commissioner's rules pursuant thereto (including 37 CFR §1.14 with particular reference to 886 OG 638).

The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in

contravention of the rights granted under the authority of any government in accordance with its patent laws.

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

WHAT IS CLAIMED IS:

1. Isolated nucleic acid comprising DNA having at least an 80% sequence identity to (a) a DNA molecule encoding a PRO363 polypeptide comprising the sequence of amino acid residues 1 to 373 of Figure 2 (SEQ ID NO:3), or (b) the complement of the DNA molecule of (a).

2. The nucleic acid of Claim 1, wherein said DNA comprises the nucleotide sequence of SEQ ID NO:1 or its complement.

3. The nucleic acid of Claim 1, wherein said DNA comprises nucleotides 190-1308 of the nucleotide sequence of SEQ ID NO:1 (SEQ ID NO:2).

4. Isolated nucleic acid comprising DNA having at least an 80% sequence identity to (a) a DNA molecule encoding the same mature polypeptide encoded by the human protein cDNA in ATCC Deposit No. ______________________ (DNA45419-1252), or (b) the complement of the DNA molecule of (a).

5. The nucleic acid of Claim 4 which comprises a DNA molecule encoding the same mature polypeptide encoded by the human protein cDNA in ATCC Deposit No. ___________ (DNA45419-1252).

6. Isolated nucleic acid comprising DNA having at least an 80% sequence identity to (a) a DNA molecule encoding a PRO363 polypeptide comprising the sequence of amino acid residues 1 to X of Figure 2 (SEQ ID NO:3), or (b) the complement of the DNA molecule of (a), wherein X is any one of amino acid residues 216-225 of Figure 2 (SEQ ID NO:3).

7. A vector comprising the nucleic acid of any one of Claims 1 to 7.

8. The vector of Claim 7 operably linked to control sequences recognized by a host cell transformed with the vector.

9. A host cell comprising the vector of Claim 7.

10. The host cell of Claim 9, wherein said cell is a CHO cell.

11. The host cell of Claim 9, wherein said cell is an *E. coli*.

12. The host cell of Claim 9, wherein said cell is a yeast cell.

13. A process for producing a PRO363 polypeptide comprising culturing the host cell of Claim 9 under conditions suitable for expression of said PRO363 polypeptide and recovering said PRO363 polypeptide from the cell culture.

14. Isolated native sequence PRO363 polypeptide comprising amino acid residues 1 to 373 of Figure 2 (SEQ ID NO:3).

15. Isolated PRO363 polypeptide comprising amino acids 1 to X of the amino acid sequence shown in Figure 2 (SEQ ID NO:3), wherein X is any one of amino acids 216-225.

16. Isolated PRO363 polypeptide encoded by the cDNA insert of the vector deposited as ATCC Accession No. ______________ (DNA45419-1252).

17. A chimeric molecule comprising a PRO363 polypeptide fused to a heterologous amino acid sequence.

18. The chimeric molecule of Claim 17, wherein said heterologous amino acid sequence is an epitope tag sequence.

19. The chimeric molecule of Claim 17, wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

20. An antibody which specifically binds to a PRO363 polypeptide.

21. The antibody of Claim 20, wherein said antibody is a monoclonal antibody.

Abstract of the Disclosure

The present invention is directed to novel polypeptides having homology to the membrane-bound protein HCAR and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

FIGURE 1A

```
  1 GCGCCGGGAG CCCATCTGCC CCCAGGGGCA CGGGGCGCGG GGCCGGCTCC CGCCCGGCAC ATGGCTGCAG CCACCTCGCG CGCACCCCGA GGCGCCGCGC
    CGCGGCCCTC GGGTAGACGG GGGTCCCCGT GCCCCGCGCC CCGGCCGAGG GCGGGCCGTG TACCGACGTC GGTGGAGCGC GCGTGGGGCT CCGCGGCGCG

101 CCAGCTCGCC CGAGGTCCGT CGGAGGCGCC CGGCCGCCCC GGAGCCAAGC AGCAACTGAG CGGGGAAGCG CCCGCGTCCG GGGATCGGGA TGTCCCTCCT
    GGTCGAGCGG GCTCCAGGCA GCCTCCGCGG GCCGGCGGGG CCTCGGTTCG TCGTTGACTC GCCCCTTCGC GGGCGCAGGC CCCTAGCCCT ACAGGGAGGA
  1                                                                                                   M  S  L  L
                                                                                                     ^MET

201 CCTTCTCCTC TTGCTAGTTT CCTACTATGT TGGAACCTTG GGGACTCACA CTGAGATCAA GAGAGTGGCA GAGGAAAAGG TCACTTTGCC CTGCCACCAT
    GGAAGAGGAG AACGATCAAA GGATGATACA ACCTTGGAAC CCCTGAGTGT GACTCTAGTT CTCTCACCGT CTCCTTTTCC AGTGAAACGG GACGGTGGTA
  5  L  L  L   L  L  V  S   Y  Y  V   G  T  L   G  T  H  T   E  I  K   R  V  A   E  E  K  V   T  L  P   C  H  H

301 CAACTGGGGC TTCCAGAAAA AGACACTCTG GATATTGAAT GGCTGCTCAC CGATAATGAA GGGAACCAAA AAGTGGTGAT CACTTACTCC AGTCGTCATG
    GTTGACCCCG AAGGTCTTTT TCTGTGAGAC CTATAACTTA CCGACGAGTG GCTATTACTT CCCTTGGTTT TTCACCACTA GTGAATGAGG TCAGCAGTAC
 38 Q  L  G  L   P  E  K   D  T  L   D  I  E  W   L  L  T   D  N  E   G  N  Q  K   V  V  I   T  Y  S   S  R  H  V

401 TCTACAATAA CTTGACTGAG GAACAGAAGG GCCGAGTGGC CTTTGCTTCC AATTTCCTGG CAGGAGATGC CTCCTTGCAG ATTGAACCTC TGAAGCCCAG
    AGATGTTATT GAACTGACTC CTTGTCTTCC CGGCTCACCG GAAACGAAGG TTAAAGGACC GTCCTCTACG GAGGAACGTC TAACTTGGAG ACTTCGGGTC
 72  Y  N  N   L  T  E   E  Q  K  G   R  V  A   F  A  S   N  F  L  A   G  D  A   S  L  Q   I  E  P  L   K  P  S

501 TGATGAGGGC CGGTACACCT GTAAGGTTAA GAATTCAGGG CGCTACGTGT GGAGCCATGT CATCTTAAAA GTCTTAGTGA GACCATCCAA GCCCAAGTGT
    ACTACTCCCG GCCATGTGGA CATTCCAATT CTTAAGTCCC GCGATGCACA CCTCGGTACA GTAGAATTTT CAGAATCACT CTGGTAGGTT CGGGTTCACA
105  D  E  G   R  Y  T  C   K  V  K   N  S  G   R  Y  V  W   S  H  V   I  L  K   V  L  V  R   P  S  K   P  K  C

601 GAGTTGGAAG GAGAGCTGAC AGAAGGAAGT GACCTGACTT TGCAGTGTGA GTCATCCTCT GGCACAGAGC CCATTGTGTA TTACTGGCAG CGAATCCGAG
    CTCAACCTTC CTCTCGACTG TCTTCCTTCA CTGGACTGAA ACGTCACACT CAGTAGGAGA CCGTGTCTCG GGTAACACAT AATGACCGTC GCTTAGGCTC
138 E  L  E  G   E  L  T   E  G  S   D  L  T  L   Q  C  E   S  S  S   G  T  E  P   I  V  Y   Y  W  Q   R  I  R  E

701 AGAAAGAGGG AGAGGATGAA CGTCTGCCTC CCAAATCTAG GATTGACTAC AACCACCCTG GACGAGTTCT GCTGCAGAAT CTTACCATGT CCTACTCTGG
    TCTTTCTCCC TCTCCTACTT GCAGACGGAG GGTTTAGATC CTAACTGATG TTGGTGGGAC CTGCTCAAGA CGACGTCTTA GAATGGTACA GGATGAGACC
172  K  E  G   E  D  E   R  L  P  P   K  S  R   I  D  Y   N  H  P  G   R  V  L   L  Q  N   L  T  M  S   Y  S  G

801 ACTGTACCAG TGCACAGCAG GCAACGAAGC TGGGAAGGAA AGCTGTGTGG TGCGAGTAAC TGTACAGTAT GTACAAAGCA TCGGCATGGT TGCAGGAGCA
    TGACATGGTC ACGTGTCGTC CGTTGCTTCG ACCCTTCCTT TCGACACACC ACGCTCATTG ACATGTCATA CATGTTTCGT AGCCGTACCA ACGTCCTCGT
205  L  Y  Q   C  T  A  G   N  E  A   G  K  E   S  C  V  V   R  V  T   V  Q  Y   V  Q  S  I   G  M  V   A  G  A
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FIGURE 1B

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 901 GTGACAGGCA TAGTGGCTGG AGCCCTGCTG ATTTTCCTCT TGGTGTGGCT GCTAATCCGA AGGAAAGACA AAGAAAGATA TGAGGAAGAA GAGAGACCTA
     CACTGTCCGT ATCACCGACC TCGGGACGAC TAAAAGGAGA ACCACACCGA CGATTAGGCT TCCTTTCTGT TTCTTTCTAT ACTCCTTCTT CTCTCTGGAT
 238 V  T  G  I   V  A  G   A  L  L   I  F  L  L   V  W  L   L  I  R   R  K  D  K   E  R  Y   E  E  E   E  R  P  N

1001 ATGAAATTCG AGAAGATGCT GAAGCTCCAA AAGCCCGTCT TGTGAAACCC AGCTCCTCTT CCTCAGGCTC TCGGAGCTCA CGCTCTGGTT CTTCCTCCAC
     TACTTTAAGC TCTTCTACGA CTTCGAGGTT TTCGGGCAGA ACACTTTGGG TCGAGGAGAA GGAGTCCGAG AGCCTCGAGT GCGAGACCAA GAAGGAGGTG
 272  E  I  R   E  D  A   E  A  P  K   A  R  L   V  K  P   S  S  S  S   S  G  S   R  S  S   R  S  G  S   S  S  T

1101 TCGCTCCACA GCAAATAGTG CCTCACGCAG CCAGCGGACA CTGTCAACTG ACGCAGCACC CCAGCCAGGG CTGGCCACCC AGGCATACAG CCTAGTGGGG
     AGCGAGGTGT CGTTTATCAC GGAGTGCGTC GGTCGCCTGT GACAGTTGAC TGCGTCGTGG GGTCGGTCCC GACCGGTGGG TCCGTATGTC GGATCACCCC
 305  R  S  T   A  N  S  A   S  R  S   Q  R  T   L  S  T  D   A  A  P   Q  P  G   L  A  T  Q   A  Y  S   L  V  G

1201 CCAGAGGTGA GAGGTTCTGA ACCAAAGAAA GTCCACCATG CTAATCTGAC CAAAGCAGAA ACCACACCCA GCATGATCCC CAGCCAGAGC AGAGCCTTCC
     GGTCTCCACT CTCCAAGACT TGGTTTCTTT CAGGTGGTAC GATTAGACTG GTTTCGTCTT TGGTGTGGGT CGTACTAGGG GTCGGTCTCG TCTCGGAAGG
 338 P  E  V  R   G  S  E   P  K  K   V  H  H  A   N  L  T   K  A  E   T  T  P  S   M  I  P   S  Q  S   R  A  F  Q

1301 AAACGGTCTG AATTACAATG GACTTGACTC CCACGCTTTC CTAGGAGTCA GGGTCTTTGG ACTCTTCTCG TCATTGGAGC TCAAGTCACC AGCCACACAA
     TTTGCCAGAC TTAATGTTAC CTGAACTGAG GGTGCGAAAG GATCCTCAGT CCCAGAAACC TGAGAAGAGC AGTAACCTCG AGTTCAGTGG TCGGTGTGTT
 372  T  V  O

1401 CCAGATGAGA GGTCATCTAA GTAGCAGTGA GCATTGCACG GAACAGATTC AGATGAGCAT TTTCCTTATA CAATACCAAA CAAGCAAAAG GATGTAAGCT
     GGTCTACTCT CCAGTAGATT CATCGTCACT CGTAACGTGC CTTGTCTAAG TCTACTCGTA AAAGGAATAT GTTATGGTTT GTTCGTTTTC CTACATTCGA

1501 GATTCATCTG TAAAAAGGCA TCTTATTGTG CCTTTAGACC AGAGTAAGGG AAAGCAGGAG TCCAAATCTA TTTGTTGACC AGGACCTGTG GTGAGAAGGT
     CTAAGTAGAC ATTTTTCCGT AGAATAACAC GGAAATCTGG TCTCATTCCC TTTCGTCCTC AGGTTTAGAT AAACAACTGG TCCTGGACAC CACTCTTCCA

1601 TGGGGAAAGG TGAGGTGAAT ATACCTAAAA CTTTTAATGT GGGATATTTT GTATCAGTGC TTTGATTCAC AATTTTCAAG AGGAAATGGG ATGCTGTTTG
     ACCCCTTTCC ACTCCACTTA TATGGATTTT GAAAATTACA CCCTATAAAA CATAGTCACG AAACTAAGTG TTAAAAGTTC TCCTTTACCC TACGACAAAC

1701 TAAATTTTCT ATGCATTTCT GCAAACTTAT TGGATTATTA GTTATTCAGA CAGTCAAGCA GAACCCACAG CCTTATTACA CCTGTCTACA CCATGTACTG
     ATTTAAAAGA TACGTAAAGA CGTTTGAATA ACCTAATAAT CAATAAGTCT GTCAGTTCGT CTTGGGTGTC GGAATAATGT GGACAGATGT GGTACATGAC

1801 AGCTAACCAC TTCTAAGAAA CTCCAAAAAA GGAAACATGT GTCTTCTATT CTGACTTAAC TTCATTTGTC ATAAGGTTTG GATATTAATT TCAAGGGGAG
     TCGATTGGTG AAGATTCTTT GAGGTTTTTT CCTTTGTACA CAGAAGATAA GACTGAATTG AAGTAAACAG TATTCCAAAC CTATAATTAA AGTTCCCCTC

1901 TTGAAATAGT GGGAGATGGA GAAGAGTGAA TGAGTTTCTC CCACTCTATA CTAATCTCAC TATTTGTATT GAGCCCAAAA TAACTATGAA AGGAGACAAA
     AACTTTATCA CCCTCTACCT CTTCTCACTT ACTCAAAGAG GGTGAGATAT GATTAGAGTG ATAAACATAA CTCGGGTTTT ATTGATACTT TCCTCTGTTT

2001 AATTTGTGAC AAAGGATTGT GAAGAGCTTT CCATCTTCAT GATGTTATGA GGATTGTTGA CAAACATTAG AAATATATAA TGGAGCAATT GTGGATTTCC
     TTAAACACTG TTTCCTAACA CTTCTCGAAA GGTAGAAGTA CTACAATACT CCTAACAACT GTTTGTAATC TTTATATATT ACCTCGTTAA CACCTAAAGG

2101 CCTCAAATCA GATGCCTCTA AGGACTTTCC TGCTAGATAT TTCTGGAAGG AGAAAATACA ACATGTCATT TATCAACGTC CTTAGAAAGA ATTCTTCTAG
     GGAGTTTAGT CTACGGAGAT TCCTGAAAGG ACGATCTATA AAGACCTTCC TCTTTTATGT TGTACAGTAA ATAGTTGCAG GAATCTTTCT TAAGAAGATC
```

FIGURE 1C

```
2201 AGAAAAAGGG ATCTAGGAAT GCTGAAAGAT TACCCAACAT ACCATTATAG TCTCTTCTTT CTGAGAAAAT GTGAAACCAG AATTGCAAGA CTGGGTGGAC
     TCTTTTTCCC TAGATCCTTA CGACTTTCTA ATGGGTTGTA TGGTAATATC AGAGAAGAAA GACTCTTTTA CACTTTGGTC TTAACGTTCT GACCCACCTG

2301 TAGAAAGGGA GATTAGATCA GTTTTCTCTT AATATGTCAA GGAAGGTAGC CGGGCATGGT GCCAGGCACC TGTAGGAAAA TCCAGCAGGT GGAGGTTGCA
     ATCTTTCCCT CTAATCTAGT CAAAAGAGAA TTATACAGTT CCTTCCATCG GCCCGTACCA CGGTCCGTGG ACATCCTTTT AGGTCGTCCA CCTCCAACGT

2401 GTGAGCCGAG ATTATGCCAT TGCACTCCAG CCTGGGTGAC AGAGCGGGAC TCCGTCTC
     CACTCGGCTC TAATACGGTA ACGTGAGGTC GGACCCACTG TCTCGCCCTG AGGCAGAG
```

FIGURE 2

```
1   MSLLLLLLLV SYYVGTLGTH TEIKRVAEEK VTLPCHHQLG LPEKDTLDIE WLLTDNEGNQ KVVITYSSRH VYNNLTEEQK GRVAFASNFL AGDASLQIEP

101 LKPSDEGRYT CKVKNSGRYV WSHVILKVLV RPSKPKCELE GELTEGSDLT LQCESSSGTE PIVYYWQRIR EKEGEDERLP PKSRIDYNHP GRVLLQNLTM

201 SYSGLYQCTA GNEAGKESCV VRVTVQYVQS IGMVAGAVTG IVAGALLIFL LVWLLIRRKD KERYEEEERP NEIREDAEAP KARLVKPSSS SSGSRSSRSG
                      ^Transmembrane domain

301 SSSTRSTANS ASRSQRTLST DAAPQPGLAT QAYSLVGPEV RGSEPKKVHH ANLTKAETTP SMIPSQSRAF QTV
```

FIGURE 3A

```
3171185          1 ATTTTTAAAAATCAACTTTTATTCTACTCAAAAAAAAANAANNAAACAAA
3522954          1                                        ACTACAACCAC
1719635          1                                            CAACCAC
                   eeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeee+....+++.+.
<consen01>       1 ATTTTTAAAAATCAACTTTTATTCTACTCAAAAAAAAANACTACAACCAC

3171185         51 ACAAACAAACCTGCAAATACTCATTCTGTCCAGAGCTTATGTTTTTTGAG
3522954         12 CCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA
1719635          8 CCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA
AA318060         1                                    CTACTCTGGACTGTA
                   .+......+..+..........++..+..+..+..++..+.+....++..
<consen01>      51 CCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA

3171185        101 TTAATAACATATTTCCTAGCTTACGTTTGGTTTTACTTGTGCTTTTGCTT
3522954         62 CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAG
1719635         58 CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAG
AA318060        16 CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAG
AA373427         1                                                 AG
                   ..+.+..........+.+.....+..........+..++++...+.....
<consen01>     101 CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAG

3171185        151 CTGAGAAAATAGATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACA
3522954        112 TAACTGTACAGTATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACA
1719635        108 TAACTGTACAGTATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACA
AA318060        66 TAACTGTACAGTATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACA
AA373427         3 TAACTGTACAGTATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACA
2811116          1                                    GCAGGAGCAGTGACA
2812338          1                                    GCAGGAGCAGTGACA
                   .......+....++++++++++++++++++++++++++++++++++++++
<consen01>     151 TAACTGTACAGTATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACA

3171185        201 GGCATAGTGGCTGGAGCCCTGCTGATTTTCC-TCTTGGTGTGGCTGCTAA
3522954        162 GGCATA-TGGCTGGAGCC-TGNCGNNTTTCCCTCTGGGTG-GGCTGTNCT
1719635        158 GGCATAGTGGCTGGAGCCCTGCTGATTTTCC-TCTTGGTGTGGCTGCTAA
AA318060       116 GGCATAGTGGCTGGAGCCCTGCTGATTTTCC-TCTTGGTGTGGCTGCTAA
AA373427        53 GGCATAGTGGCTGGAGCCCTGCTGATTTTCC-TCTTGGTGTGGCTGCTAA
2811116         16 GGCATAGTGGGTGGAGCCCTGCTGATTTTCC-TCTTGGTGTGGCTGCTAA
2812338         16 GGCATAGTGGCTGGAGCCCTGCTGANTTTCC-TCTTGGTGTGGCTGCTAA
                   ++++++++++.++++++++++..+..+++++ +++.++++++++++....
<consen01>     201 GGCATAGTGGCTGGAGCCCTGCTGATTTTCC TCTTGGTGTGGCTGCTAA

3171185        250 TCCGAAG-AAAGACAAAGAAA
3522954        209 NCGAGNANNANAAA
1719635        207 TCCGAAG-AAAGACAAAGAA
AA318060       165 TCCGAAG-AAAGACAAAGAAAGATATGAGGAAGAAGAGAGACCTAATGAA
AA373427       102 TCCGAAG-AAAGACAAAGAAAGATATGAGGAAGAAGAGAGACCTAATGAA
2811116         65 TCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGAGAGACCTAATGAA
2812338         65 TCCGAAG-AAAGACAAAGAAAGATATGAGGAAGAAGAGAGACCTAATGAA
                   .+.......+..+.++++++++++++++++++++++++++++++++++++
<consen01>     250 TCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGAGAGACCTAATGAA
```

FIGURE 3B

```
AA318060      214 ATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTNTTGTGAAACCCAGCTC
AA373427      151 ATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTTTTGTGAA-CCCAGCTC
2811116       115 ATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCTC
2812338       114 ATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCTC
046867          1                    GTTTCACAAGACGGGCTTTTGGAGCCCAGCTC
                  +++++++++++++++++.+.++.+++.+.+..++.++.+.++++++++
<consen01>    300 ATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCTC

AA318060      264 CTCTTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCCTCCACTTCGC
AA373427      200 CTCTTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCCTCCACT-CGC
2811116       165 CTCTTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCCTCCACT-CG-
2812338       164 CTCTTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCCTCCACT-CGC
046867         33 CTCTTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCCTCCACT-CGC
                  ++++++++++++++++++++++++++++++++++++++++++++++ +++
<consen01>    350 CTCTTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCCTCCACT CGC

AA318060      314 TCCACAGCAAATAGTGCCT
AA373427      249 TCCACAGCAAATAGTGCCTCACGCAGCCAGCGGACACTGTCAA-CTGACG
2811116       213 TCCACAGCAAATAGTGCCTCACGCAGCCAGCGGACACTGTCAAACTGACG
2812338       213 TCCACAGCAAATAGTGCCTCACGCAGCCAGCGGACACTGTCAA-CTGACG
046867         82 TCCACAGCAAATAGTGCCTCACGCAGCCAGCGGACACTGTNAA-CTNACG
046343          1                                 GACAGTNTCCG-NTGACG
                  ++++++++++++++++++++++++++++++++++.+.+...  .+.+++
<consen01>    399 TCCACAGCAAATAGTGCCTCACGCAGCCAGCGGACACTGTCAA CTGACG

AA373427      298 CAGCACCCCAGNCAGGGCTGGCCCACCCAGG
2811116       263 CAGCACCCCAGCCAGG-CTGGCC-ACC-AGGCATACAGCTATGGGCAGAG
2812338       262 CAGCACCCCAGCCAGGN-TGGCC-ACC-AGGCATACAGCCTAGTGG
046867        131 CAGCACCCCAGCCAGGGCTGGCC-ACCCAGGCATACAGCCTAGTGGGGCC
046343         18 CAGCACCCCAGCCAGGGCTGGCC-ACCCAGGCATACAGCCTAGTGGGGCC
                  +++++++++++.++++.++++++++++++++++++++...+.+..+..
<consen01>    448 CAGCACCCCAGCCAGGGCTGGCCCACCCAGGCATACAGCCTAGTGGGGCC

2811116       310 TG
046867        180 AGAGGTGNGAGGTTCTNAACCAAAGAAAGTCCACCATGCTAATCTNACCA
046343         67 AGAGGTGAGAGGTTCTGAACCAAAGAAAGTNCACCATGCTAATCTGACCA
                  .++++++.++++++++.++++++++++++.+++++++++++++.++++
<consen01>    498 AGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATGCTAATCTGACCA

046867        230 AAGCAGAAACCACACCCAGCATGNTCCTCAT
046343        117 AAGCAGAAACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA
                  ++++++++++++++++++++++.+++.++.eeeeeeeeeeeeeeeeeee
<consen01>    548 AAGCAGAAACCACACCCAGCATGATCCTCATCCAGAGCAGAGCCTTCCAA

046343        167 ACGGTCTGAATTACAATNGACTTNNCTNCCACGCTTTC
                  eeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeee
<consen01>    598 ACGGTCTGAATTACAATNGACTTNNCTNCCACGCTTTC
```

FIGURE 4

```
  1 ATTTTTAAAA ATCAACTTTT ATTCTACTCA AAAAAAAANA CTACAACCAC CCTGGACGAG TTCTGCTGCA GAATCTTACC ATGTCCTACT CTGGACTGTA
    TAAAAATTTT TAGTTGAAAA TAAGATGAGT TTTTTTTTNT GATGTTGGTG GGACCTGCTC AAGACGACGT CTTAGAATGG TACAGGATGA GACCTGACAT
  1         K  S  T  F   I  L  L  K   K  K  X   Y  N  H   P  G  R  V   L  L  Q   N  L  T   M  S  Y  S   G  L  Y
            ^orf

101 CCAGTGCACA GCAGGCAACG AAGCTGGGAA GGAAAGCTGT GTGGTGCGAG TAACTGTACA GTATGTACAA AGCATCGGCA TGGTTGCAGG AGCAGTGACA
    GGTCACGTGT CGTCCGTTGC TTCGACCCTT CCTTTCGACA CACCACGCTC ATTGACATGT CATACATGTT TCGTAGCCGT ACCAACGTCC TCGTCACTGT
 32  Q  C  T   A  G  N  E   A  G  K   E  S  C   V  V  R  V   T  V  Q   Y  V  Q   S  I  G  M   V  A  G   A  V  T
    ^42828.f1                                                          ^42828.p1

201 GGCATAGTGG CTGGAGCCCT GCTGATTTTC CTCTTGGTGT GGCTGCTAAT CCGAAGGAAA GACAAAGAAA GATATGAGGA AGAAGAGAGA CCTAATGAAA
    CCGTATCACC GACCTCGGGA CGACTAAAAG GAGAACCACA CCGACGATTA GGCTTCCTTT CTGTTTCTTT CTATACTCCT TCTTCTCTCT GGATTACTTT
 65 G  I  V  A   G  A  L   L  I  F   L  L  V  W   L  L  I   R  R  K   D  K  E  R   Y  E  E   E  E  R   P  N  E  I

301 TTCGAGAAGA TGCTGAAGCT CCAAAAGCCC GTCTTGTGAA ACCCAGCTCC TCTTCCTCAG GCTCTCGGAG CTCACGCTCT GGTTCTTCCT CCACTCGCTC
    AAGCTCTTCT ACGACTTCGA GGTTTTCGGG CAGAACACTT TGGGTCGAGG AGAAGGAGTC CGAGAGCCTC GAGTGCGAGA CCAAGAAGGA GGTGAGCGAG
 99  R  E  D   A  E  A   P  K  A  R   L  V  K   P  S  S   S  S  S  G   S  R  S   S  R  S   G  S  S  S   T  R  S

401 CACAGCAAAT AGTGCCTCAC GCAGCCAGCG GACACTGTCA ACTGACGCAG CACCCCAGCC AGGGCTGGCC CACCCAGGCA TACAGCCTAG TGGGGCCAGA
    GTGTCGTTTA TCACGGAGTG CGTCGGTCGC CTGTGACAGT TGACTGCGTC GTGGGGTCGG TCCCGACCGG GTGGGTCCGT ATGTCGGATC ACCCCGGTCT
132  T  A  N   S  A  S  R   S  Q  R   T  L  S   T  D  A  A   P  Q  P   G  L  A   H  P  G  I   Q  P  S   G  A  R
                                                                                                          ^42828.r1

501 GGTGAGAGGT TCTGAACCAA AGAAAGTCCA CCATGCTAAT CTGACCAAAG CAGAAACCAC ACCCAGCATG ATCCTCATCC AGAGCAGAGC CTTCCAAACG
    CCACTCTCCA AGACTTGGTT TCTTTCAGGT GGTACGATTA GACTGGTTTC GTCTTTGGTG TGGGTCGTAC TAGGAGTAGG TCTCGTCTCG GAAGGTTTGC
165 G  E  R  F   O

601 GTCTGAATTA CAATNGACTT NNCTNCCACG CTTTC
    CAGACTTAAT GTTANCTGAA NNGANGGTGC GAAAG
```

FIGURE 5

```
MYP0_BOVIN  1       IVVYTDKEVHGAVGSQVTLYCSFWSSEWVSDDLSFTWRYQPE
                        |  |        ||| |         | |   |
  DNA45419  15      gtlgTHtEIkrvaeekVTLpChhqlglpekDtLdieWlltdn

BL00568C    A<->C   (31,31):30
MYP0_HUMAN  103     GDPRWKDGSIVIHNLDYSDNGTFTCDVKNP
                          | |  |  |  || |  || |||
  DNA45419  87      snflagDaSlqIepLkpSDeGryTCkVKNs
```